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AMENDMENTS TO THE CLAIMS

1. (withdrawn) A modified cytochrome P450 monooxygenase which, in comparison with the wild-type enzyme, shows an altered substrate profile in the terminal and/or subterminal enzymatic hydroxylation of aliphatic carboxylic acids, owing to site-specific mutagenesis of its substrate binding region.
2. (withdrawn) A monooxygenase as claimed in claim 1, which is derived from cytochrome P450 monooxygenases of bacterial origin.
3. (withdrawn) A monooxygenase as claimed in claim 2, which is derived from *Bacillus megaterium* cytochrome P450 monooxygenase BM-3 with an amino acid sequence in accordance with SEQ ID NO: 2, which has at least one functional mutation in one of the following amino acid sequence regions: 24-28, 45-51, 70-72, 73-82, 86-88, 172-224 and 352-356, with the proviso that, if the enzyme carries the mutation F87A, more than one of these regions is mutated.
4. (withdrawn) A monooxygenase as claimed in claim 3, which comprises at least one functional mutation in the amino acid sequence regions 86-88 and 172-224.
5. (withdrawn) A monooxygenase as claimed in claim 4, which comprises at least one of the following amino acid substitution patterns:
 - a) F87V;
 - b) F87A L188K;
 - c) F87V L188K;
 - d) F87A L188K A74G;
 - e) F87V L188K A74G;
 - f) F87A L188K A74G R47F;

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- g) F87V L188K A74G R47F;
 - h) F87A L188K A74G R47F V26T; or
 - i) F87V L188K A74G R47F V26T;
- and functional equivalents thereof.
6. (withdrawn) A monooxygenase as claimed in claim 3, which comprises a single amino acid substitution from amongst the following:
- a) V26T,
 - b) R47F,
 - c) S72G,
 - d) A74G,
 - e) F87V,
 - f) L188z, where Z is an amino acid selected from amongst K, R, W, Q, N, G, A and S, and
 - g) M354T;
- and functional equivalents thereof.
7. (withdrawn) A nucleic acid sequence encoding a monooxygenase as claimed in claim 1 and the complementary nucleic acid sequence thereof.
8. (withdrawn) An expression construct comprising, under the genetic control of regulatory acid sequence, an encoding sequence which encompasses a nucleic acid sequence as claimed in claim 7.
9. (withdrawn) A vector which encompasses at least one expression construct as claimed in claim 8.
10. (withdrawn) A recombinant microorganism which has been transformed with at least one

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vector as claimed in claim 9.

11. (withdrawn) A microorganism as claimed in claim 10, selected from amongst bacteria of the genus *Escherichia*.
12. (currently amended) A process for the enzymatic production of subterminally hydroxylated aliphatic carboxylic acids, which comprises
 - a) culturing a recombinant microorganism which has been transformed with a vector which encompasses an expression construct comprising, under the genetic control of regulatory nucleic acid sequences, a sequence which encompasses a nucleic acid sequence encoding a monooxygenase which is derived from *Bacillus megaterium* cytochrome P450 monooxygenase BM-3 with an amino acid sequence in accordance with SEQ ID NO: 2, which has a functional mutation in the amino acid sequence region 86-88 and optionally at least one further functional mutation in one of the following amino acid sequence regions: 24-28, 45-51, 73-82, and 172-224, with the proviso that, if the enzyme carries the mutation F87A, more than one of these regions is mutated, which functional mutation modified cytochrome P450 monooxygenase which, in comparison with the wild-type enzyme, shows an altered substrate profile results in an altered activity or regioselectivity in the subterminal enzymatic hydroxylation of aliphatic carboxylic acids, owing to site-specific mutagenesis of its substrate binding region, an aliphatic C₈-C₁₂-carboxylic acid, whereby culturing is performed in the presence of a culture medium which contains at least one hydroxylatable C₈-C₁₂-carboxylic acid or at least one hydroxylatable C₈-C₁₂-carboxylic acid a derivative thereof selected from at alkyl ester, an amide or an anhydride thereof; or

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- a2) incubating a reaction medium containing at least one hydroxylatable C₈-C₁₂-carboxylic acid or ~~at least one hydroxylatable C₈-C₁₂-carboxylic acid~~ a derivative thereof, selected from an alkyl ester, an amide or an anhydride thereof with said ~~a~~ modified monooxygenase as defined above, and
- b) isolating the resulting hydroxylated product from the medium.
13. (canceled)
14. (currently amended) A method as claimed in claim 12, wherein the hydroxylatable carboxylic acid is a C₈-C₁₂-monocarboxylic acid or a derivative thereof and the monooxygenase (~~SEQ ID NO:2~~) ~~used~~ comprises at least one of the following amino acid substitution patterns in an amino acid sequence according to SEQ ID NO: 2:
- a) F87V;
- b) F87A and L188K;
- c) F87V and L188K;
- d) F87A L188K and A74G;
- e) F87V L188K and A74G;
- f) F87A L188K A74G R47F;
- g) F87V L188K A74G R47F;
- h) F87A L188K A74G R47F V26T; or
- i) F87V L188K A74G R47F V26T.
15. (canceled)
16. (currently amended) A method a claimed in claim 12, wherein the ~~reaction~~ enzymatic production is carried out in the presence of an electron donor or a reduction equivalent.
17. (previously presented) A method as claimed in claim 16, wherein the electron donor or

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the reduction equivalent is selected from amongst NADH, NADPH and Zn/CO(III) sepulchrate.

18. (new) The process of claim 12, wherein the monooxygenase comprises at least one functional mutation in the amino acid sequence regions 86-88 and 172-224.